

=====

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2007; month=11; day=26; hr=13; min=35; sec=25; ms=131;
]

=====

Reviewer Comments:

2

23388us01

Please delete the end of file text which appears below seq id 59.

Application No: 10723908 Version No: 2.0

Input Set:**Output Set:**

Started: 2007-10-31 21:40:09.000
Finished: 2007-10-31 21:40:12.723
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 723 ms
Total Warnings: 59
Total Errors: 9
No. of SeqIDs Defined: 59
Actual SeqID Count: 59

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
W 402	Undefined organism found in <213> in SEQ ID (15)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2007-10-31 21:40:09.000
Finished: 2007-10-31 21:40:12.723
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 723 ms
Total Warnings: 59
Total Errors: 9
No. of SeqIDs Defined: 59
Actual SeqID Count: 59

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
W 213	Artificial or Unknown found in <213> in SEQ ID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
W 213	Artificial or Unknown found in <213> in SEQ ID (34)
W 213	Artificial or Unknown found in <213> in SEQ ID (35)
W 213	Artificial or Unknown found in <213> in SEQ ID (36)
W 213	Artificial or Unknown found in <213> in SEQ ID (37)
W 213	Artificial or Unknown found in <213> in SEQ ID (38)
W 213	Artificial or Unknown found in <213> in SEQ ID (39)
W 213	Artificial or Unknown found in <213> in SEQ ID (40)
W 213	Artificial or Unknown found in <213> in SEQ ID (41)
W 213	Artificial or Unknown found in <213> in SEQ ID (42)
W 213	Artificial or Unknown found in <213> in SEQ ID (43)
W 213	Artificial or Unknown found in <213> in SEQ ID (44)
W 213	Artificial or Unknown found in <213> in SEQ ID (45)
W 213	Artificial or Unknown found in <213> in SEQ ID (46)
W 213	Artificial or Unknown found in <213> in SEQ ID (48)
W 213	Artificial or Unknown found in <213> in SEQ ID (49)
W 213	Artificial or Unknown found in <213> in SEQ ID (50)
W 213	Artificial or Unknown found in <213> in SEQ ID (51)
W 213	Artificial or Unknown found in <213> in SEQ ID (52)
	This error has occurred more than 20 times, will not be displayed
E 355	Empty lines found between the amino acid numbering and the

Input Set:

Output Set:

Started: 2007-10-31 21:40:09.000
Finished: 2007-10-31 21:40:12.723
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 723 ms
Total Warnings: 59
Total Errors: 9
No. of SeqIDs Defined: 59
Actual SeqID Count: 59

Error code	Error Description
E 321	No. of Bases conflict, this line has no nucleotides SEQID (59)
E 259	Found undefined lettercode; POS (31) SEQID(59)
E 259	Found undefined lettercode; POS (32) SEQID(59)
E 259	Found undefined lettercode; POS (33) SEQID(59)
E 259	Found undefined lettercode; POS (34) SEQID(59)
E 259	Found undefined lettercode; POS (35) SEQID(59)
E 254	The total number of bases conflicts with running total, Input: 1, Calculated : 37 SEQID(59)
E 253	The number of bases differs from <211> Input: 30 Calculated:37

SEQUENCE LISTING

<110> Statens Serum Institut

<120> Tuberculosis vaccine and diagnostics
based on the Mycobacterium tuberculosis esat-6 gene family

<130> 23388us1

<140> 10723908

<141> 2007-10-31

<160> 59

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 100

<212> PRT

<213> M.Tuberculosis

<400> 1

```
Met Ala Glu Met Lys Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly
 1             5             10             15
Asn Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val
      20             25             30
Glu Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly
      35             40             45
Thr Ala Ala Gln Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys
      50             55             60
Gln Lys Gln Glu Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly
65             70             75             80
Val Gln Tyr Ser Arg Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser
      85             90             95
Gln Met Gly Phe
      100
```

<210> 2

<211> 95

<212> PRT

<213> M.Tuberculosis

<400> 2

```
Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser
 1             5             10             15
Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly
      20             25             30
Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser
      35             40             45
Glu Ala Tyr Gln Gly Val Gln Gln Lys Trp Asp Ala Thr Ala Thr Glu
      50             55             60
Leu Asn Asn Ala Leu Gln Asn Leu Ala Arg Thr Ile Ser Glu Ala Gly
65             70             75             80
Gln Ala Met Ala Ser Thr Glu Gly Asn Val Thr Gly Met Phe Ala
      85             90             95
```

<210> 3
 <211> 96
 <212> PRT
 <213> M.Tuberculosis

 <400> 3
 Met Ser Gln Ile Met Tyr Asn Tyr Pro Ala Met Leu Gly His Ala Gly
 1 5 10 15
 Asp Met Ala Gly Tyr Ala Gly Thr Leu Gln Ser Leu Gly Ala Glu Ile
 20 25 30
 Ala Val Glu Gln Ala Ala Leu Gln Ser Ala Trp Gln Gly Asp Thr Gly
 35 40 45
 Ile Thr Tyr Gln Ala Trp Gln Ala Gln Trp Asn Gln Ala Met Glu Asp
 50 55 60
 Leu Val Arg Ala Tyr His Ala Met Ser Ser Thr His Glu Ala Asn Thr
 65 70 75 80
 Met Ala Met Met Ala Arg Asp Thr Ala Glu Ala Ala Lys Trp Gly Gly
 85 90 95

<210> 4
 <211> 294
 <212> DNA
 <213> M Tuberculosis

<220>
 <221> CDS
 <222> (1)...(294)

<400> 4
 atg agc ctt ttg gat gct cat atc cca cag ttg gtg gcc tcc cag tcg 48
 Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
 1 5 10 15

 gcg ttt gcc gcc aag gcg ggg ctg atg cgg cac acg atc ggt cag gcc 96
 Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
 20 25 30

 gag cag gcg gcg atg tcg gct cag gcg ttt cac cag ggg gag tcg tcg 144
 Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
 35 40 45

 gcg gcg ttt cag gcc gcc cat gcc cgg ttt gtg gcg gcg gcc gcc aaa 192
 Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys
 50 55 60

 gtc aac acc ttg ttg gat gtc gcg cag gcg aat ctg ggt gag gcc gcc 240
 Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
 65 70 75 80

 ggt acc tat gtg gcc gcc gat gct gcg gcc gcg tcg acc tat acc ggg 288
 Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly
 85 90 95

 ttc tga 294
 Phe *

<210> 5
 <211> 97
 <212> PRT
 <213> M Tuberculosis

<400> 5
 Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
 1 5 10 15
 Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
 20 25 30
 Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
 35 40 45
 Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys
 50 55 60
 Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
 65 70 75 80
 Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ser Thr Tyr Thr Gly
 85 90 95
 Phe

<210> 6
 <211> 339
 <212> DNA
 <213> M Tuberculosis

<220>
 <221> CDS
 <222> (1)...(339)

<400> 6
 ttg atc ccc ggt cgg atg gtg ctg aac tgg gaa gat ggc etc aat gcc 48
 Leu Ile Pro Gly Arg Met Val Leu Asn Trp Glu Asp Gly Leu Asn Ala
 1 5 10 15
 ctt gtt gcg gaa ggg att gag gcc atc gtg ttt cgt act tta ggc gat 96
 Leu Val Ala Glu Gly Ile Glu Ala Ile Val Phe Arg Thr Leu Gly Asp
 20 25 30
 cag tgc tgg ttg tgg gag tcg ctg ctg ccc gac gag gtg cgc cga ctg 144
 Gln Cys Trp Leu Trp Glu Ser Leu Leu Pro Asp Glu Val Arg Arg Leu
 35 40 45
 ccc gag gaa ctg gcc cgg gtg gac gca ttg ttg gac gat ccg gcg ttc 192
 Pro Glu Glu Leu Ala Arg Val Asp Ala Leu Leu Asp Asp Pro Ala Phe
 50 55 60
 ttc gcc ccg ttc gtg ccg ttc ttc gac ccg cgc agg ggc cgg ccg tcg 240
 Phe Ala Pro Phe Val Pro Phe Phe Asp Pro Arg Arg Gly Arg Pro Ser
 65 70 75 80
 acg ccg atg gag gtc tat ctg cag ttg atg ttt gtg aag ttc cgc tac 288
 Thr Pro Met Glu Val Tyr Leu Gln Leu Met Phe Val Lys Phe Arg Tyr
 85 90 95
 cgg ctg ggc tat gag tcg ctg tgc cgg gag gtg gct gat tcg atc acc 336

Arg Leu Gly Tyr Glu Ser Leu Cys Arg Glu Val Ala Asp Ser Ile Thr
 100 105 110

tga 339

<210> 7
 <211> 112
 <212> PRT
 <213> M Tuberculosis

<400> 7
 Met Ile Pro Gly Arg Met Val Leu Asn Trp Glu Asp Gly Leu Asn Ala
 1 5 10 15
 Leu Val Ala Glu Gly Ile Glu Ala Ile Val Phe Arg Thr Leu Gly Asp
 20 25 30
 Gln Cys Trp Leu Trp Glu Ser Leu Leu Pro Asp Glu Val Arg Arg Leu
 35 40 45
 Pro Glu Glu Leu Ala Arg Val Asp Ala Leu Leu Asp Asp Pro Ala Phe
 50 55 60
 Phe Ala Pro Phe Val Pro Phe Phe Asp Pro Arg Arg Gly Arg Pro Ser
 65 70 75 80
 Thr Pro Met Glu Val Tyr Leu Gln Leu Met Phe Val Lys Phe Arg Tyr
 85 90 95
 Arg Leu Gly Tyr Glu Ser Leu Cys Arg Glu Val Ala Asp Ser Ile Thr
 100 105 110

<210> 8
 <211> 285
 <212> DNA
 <213> M Tuberculosis

<220>
 <221> CDS
 <222> (1)...(285)

<400> 8
 atg acc atc aac tat caa ttc ggg gac gtc gac gct cac ggc gcc atg 48
 Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
 1 5 10 15
 atc cgc gct cag gcc ggg tcg ctg gag gcc gag cat cag gcc atc att 96
 Ile Arg Ala Gln Ala Gly Ser Leu Glu Ala Glu His Gln Ala Ile Ile
 20 25 30
 tct gat gtg ttg acc gcg agt gac ttt tgg ggc ggc gcc ggt tcg gcg 144
 Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
 35 40 45
 gcc tgc cag ggg ttc att acc cag ctg ggc cgt aac ttc cag gtg atc 192
 Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
 50 55 60
 tac gag cag gcc aac gcc cac ggg cag aag gtg cag gct gcc ggc aac 240
 Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
 65 70 75 80
 aac atg gca caa acc gac agc gcc gtc ggc tcc agc tgg gcc taa 285

Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala *

85 90

<210> 9
<211> 94
<212> PRT
<213> M Tuberculosis

<400> 9
Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
1 5 10 15
Ile Arg Ala Gln Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Val
20 25 30
Arg Asp Val Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val
35 40 45
Ala Cys Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
50 55 60
Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
65 70 75 80
Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
85 90

<210> 10
<211> 285
<212> DNA
<213> M Tuberculosis

<220>
<221> CDS
<222> (1)...(282)

<400> 10
atg acc atc aac tat cag ttc ggt gat gtc gac gct cat ggc gcc atg 48
Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
1 5 10 15
atc cgc gct cag gcc ggg ttg ctg gag gcg gag cat cag gcc atc gtt 96
Ile Arg Ala Gln Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Val
20 25 30
cgt gat gtg ttg gcc gcg ggt gac ttt tgg ggc ggc gcc ggt tcg gtg 144
Arg Asp Val Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val
35 40 45
gct tgc cag gag ttc att acc cag ttg ggc cgt aac ttc cag gtg atc 192
Ala Cys Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
50 55 60
tac gag cag gcc aac gcc cac ggg cag aag gtg cag gct gcc ggc aac 240
Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
65 70 75 80
aac atg gca caa acc gac agc gcc gtc ggc tcc agc tgg gcc 282
Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
85 90

<210> 11

<211> 94

<212> PRT

<213> M Tuberculosis

<400> 11

```

Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
 1             5             10             15
Ile Arg Ala Gln Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Val
      20             25             30
Arg Asp Val Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val
      35             40             45
Ala Cys Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
      50             55             60
Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
65             70             75             80
Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
      85             90

```

<210> 12

<211> 327

<212> DNA

<213> M Tuberculosis

<220>

<221> CDS

<222> (1)...(327)

<400> 12

```

gtg ctt ttg cct ctt ggt ccg cct ttg ccg ccc gac gcg gtg gtg gcg      48
Val Leu Leu Pro Leu Gly Pro Pro Leu Pro Pro Asp Ala Val Val Ala
 1             5             10             15

aaa cgg gct gag tcg gga atg ctc ggc ggg ttg tcg gtt ccg ctc agc      96
Lys Arg Ala Glu Ser Gly Met Leu Gly Gly Leu Ser Val Pro Leu Ser
      20             25             30

tgg gga gtg gct gtg cca ccc gat gat tat gac cac tgg gcg cct gcg      144
Trp Gly Val Ala Val Pro Pro Asp Asp Tyr Asp His Trp Ala Pro Ala
      35             40             45

ccg gag gac ggc gcc gat gtc gat gtc cag gcg gcc gaa ggg gcg gac      192
Pro Glu Asp Gly Ala Asp Val Asp Val Gln Ala Ala Glu Gly Ala Asp
      50             55             60

gca gag gcc gcg gcc atg gac gag tgg gat gag tgg cag gcg tgg aac      240
Ala Glu Ala Ala Ala Met Asp Glu Trp Asp Glu Trp Gln Ala Trp Asn
      65             70             75             80

gag tgg gtg gcg gag aac gct gaa ccc cgc ttt gag gtg cca cgg agt      288
Glu Trp Val Ala Glu Asn Ala Glu Pro Arg Phe Glu Val Pro Arg Ser
      85             90             95

agc agc agc gtg att ccg cat tct ccg gcg gcc ggc tag      327
Ser Ser Ser Val Ile Pro His Ser Pro Ala Ala Gly  *

```

<210> 13

<211> 108

<212> PRT

<213> M Tuberculosis

<400> 13

```

Met Leu Leu Pro Leu Gly Pro Pro Leu Pro Pro Asp Ala Val Val Ala
 1             5             10             15
Lys Arg Ala Glu Ser Gly Met Leu Gly Gly Leu Ser Val Pro Leu Ser
          20             25             30
Trp Gly Val Ala Val Pro Pro Asp Asp Tyr Asp His Trp Ala Pro Ala
          35             40             45
Pro Glu Asp Gly Ala Asp Val Asp Val Gln Ala Ala Glu Gly Ala Asp
          50             55             60
Ala Glu Ala Ala Ala Met Asp Glu Trp Asp Glu Trp Gln Ala Trp Asn
65             70             75             80
Glu Trp Val Ala Glu Asn Ala Glu Pro Arg Phe Glu Val Pro Arg Ser
          85             90             95
Ser Ser Ser Val Ile Pro His Ser Pro Ala Ala Gly
          100             105

```

<210> 14

<211> 324

<212> DNA

<213> M Tuberculosis

<220>

<221> CDS

<222> (1)...(324)

<400> 14

```

ttg acc cac aag cgc act aaa cgc cag cca gcc atc gcc gca ggg etc      48
Leu Thr His Lys Arg Thr Lys Arg Gln Pro Ala Ile Ala Ala Gly Leu
 1             5             10             15

aac gcc ccg cgt cgg aat cgc gtt ggg cgg caa cat ggt tgg ccg gcc      96
Asn Ala Pro Arg Arg Asn Arg Val Gly Arg Gln His Gly Trp Pro Ala
          20             25             30

gac gtt ccg tcc gcc gag cag cgc cgc gcc caa cgg cag cgc gac etc      144
Asp Val Pro Ser Ala Glu Gln Arg Arg Ala Gln Arg Gln Arg Asp Leu
          35             40             45

gag gct atc cgc cga gcg tac gcc gag atg gtg gcg aca tca cac gaa      192
Glu Ala Ile Arg Arg Ala Tyr Ala Glu Met Val Ala Thr Ser His Glu
          50             55             60

atc gac gac gac aca gcc gaa ctg gcg ctg ttg tcg atg cat ctc gac      240
Ile Asp Asp Asp Thr Ala Glu Leu Ala Leu Leu Ser Met His Leu Asp
          65             70             75             80

gat gag cag cgc cgg ctt gag gcg ggg atg aag ctc ggc tgg cat ccg      288
Asp Glu Gln Arg Arg Leu Glu Ala Gly Met Lys Leu Gly Trp His Pro
          85             90             95

```

tat cac ttc ccc gac gaa ccc gac agc aaa cag tga	324
Tyr His Phe Pro Asp Glu Pro Asp Ser Lys Gln *	
100 105	

<210> 15
 <211> 107
 <212> PRT
 <213> M Tuberculosis

<400> 15
 Met Thr His Lys Arg Thr Lys Arg Gln Pro Ala Ile Ala Ala Gly Leu
 1 5 10 15
 Asn Ala Pro Arg Arg Asn Arg Val Gly Arg Gln His Gly Trp Pro Ala
 20 25 30
 Asp Val Pro Ser Ala Glu Gln Arg Arg Ala Gln Arg Gln Arg Asp Leu
 35 40 45
 Glu Ala Ile Arg Arg Ala Tyr Ala Glu Met Val Ala Thr Ser His Glu
 50 55 60
 Ile Asp Asp Asp Thr Ala Glu Leu Ala Leu Leu Ser Met His Leu Asp
 65 70 75 80
 Asp Glu Gln Arg Arg Leu Glu Ala Gly Met Lys Leu Gly Trp His Pro
 85 90 95
 Tyr His Phe Pro Asp Glu Pro Asp Ser Lys Gln
 100 105

<210> 16
 <211> 246
 <212> DNA
 <213> M Tuberculosis

<220>
 <221> CDS
 <222> (1)...(246)

<400> 16
 atg agc ggc cac gcg ttg gct gct cgg acg ttg ctg gcc gcc gcg gac 48
 Met Ser Gly His Ala Leu Ala Ala Arg Thr Leu Leu Ala Ala Ala Asp
 1 5 10 15
 gag ctt gtc ggc ggc ccg cca gtc gag gct tcg gcc gcc gcg ctg gcc 96
 Glu Leu Val Gly Gly Pro Pro Val Glu Ala Ser Ala Ala Ala Leu Ala
 20 25 30
 ggc gac gcc gcg ggc gca tgg cgg acc gcg gcc gtc gag ctt gcg cga 144
 Gly Asp Ala Ala Gly Ala Trp Arg Thr Ala Ala Val Glu Leu Ala Arg
 35 40 45
 gcg ttg gtc cgc gct gtg gcg gag tcg cac ggc gtc gcg gcc gtt ttg 192
 Ala Leu Val Arg Ala Val Ala Glu Ser His Gly Val Ala Ala Val Leu
 50 55 60
 ttc gcc gcg acg gcc gcc gcg gcg gcc gtc gac cgg ggt gat ccg 240
 Phe Ala Ala Thr Ala Ala Al